

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/534,279
Source: PCT
Date Processed by STIC: 05/23/2006

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 05/23/2006

PATENT APPLICATION: US/10/534,279

TIME: 14:03:58

Input Set : A:\60290-USA Sequence Listing.txt

Output Set: N:\CRF4\05232006\J534279.raw

3 <110> APPLICANT: Wu, Shilan
 4 Hayashi, Jon H.
 5 Kinne, Lyle P.
 6 Dierks, Peter M.
 8 <120> TITLE OF INVENTION: Lepidoptera Voltage-Gated Calcium Channels
 10 <130> FILE REFERENCE: FMC 60290
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/534,279
 C--> 12 <141> CURRENT FILING DATE: 2005-05-06
 12 <160> NUMBER OF SEQ ID NOS: 83
 14 <170> SOFTWARE: PatentIn version 3.2
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 5047
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Heliothis virescens
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 26 aaaatcctat tcggaggtac acaaagttca tcatcgagtg gccgcccttc gactacgcgg 180
 28 tgctgcttac catcatcgcc aactgcgtgg tgctggcgct ggaggagcat ttgcctaacg 240
 30 gcgataagac catcttagca cagaatctgg aaaagaccga ggcgtacttt ttaggaatat 300
 32 tttgtgtaga agcctcgtaa aaaatcttag ccttaggttt tgttttacac aggggatcgt 360
 34 atcttaggaa cgtttggaac atcatggatt ttttcgttgt agtaactggt atcatcacgc 420
 36 agctgccgat cgcgccagcc gacgtcgact tcaggacctt gcgtgccatt aggggtgctga 480
 38 ggccccttaa attagtatcg ggcgttccta gtctgcaagt ggtactgaag tccatcataa 540
 40 aggcgatggc gccgttgctg cagatcgccc tctgggtgct ttcgcgata gtcactcttcg 600
 42 ctatcatcgg cctcgagttc tactcagggg cgctgcataa gacttgttat aatttagaag 660
 44 atattagtga aatagtaaat gaaggcgata gtgcgacgcc gtgtaacgcg gacaacgtga 720
 46 gtttagcacc atttggggca aacgtgtgtg attatgagaa gagcacgtgt ttagagaaat 780
 48 gggagggggc gaacaggggt attacgtcct tcgacaacat cggcttcgct atgctcaccg 840
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 52 taggtagtgc gttcaactgg atttactttg tgctctcat agtattgggt tcattcttta 960
 54 tgctcaactt agttctcggg gtccttagcg gtgagttcgc taaagaaaga gagaaagtag 1020
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 60 aagaagaaaa aatgcacata atagaagcac ggagaagagc agcggccaaa aagaagttaa 1200
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 76 tcaagggtgg ctccttcggt ctatctgtcc tgagagctct aagactgttg aggatattta 1680

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82	gcatgcagct	gttcggggga	cagttcaact	tcgaggacgg	cacgccgccg	accaacttca	1860
84	acacctttcc	tatcgcttg	ttactgtct	tccagatcct	aacagggtgaa	gattggaacg	1920
86	aagtgatgta	tgacggcatc	cagtcacagg	gcggcatcca	gagaggcatg	atctactctc	1980
88	tatactttgt	catcctcgtc	ttatttgga	actacacgct	gctgaacgtg	ttccttgcta	2040
90	tcgctgtcga	caacttggct	aacgcccgag	aattgacggc	ggcagaagag	gaacaagtcg	2100
92	aggaggacaa	ggagaaacag	ctccaggaat	tggagaaagg	gatgggtgca	ttacacgcgg	2160
94	tggacggcac	tccaccggga	gtagatctaa	gtccctcttc	gccgacgagt	aggaagaaca	2220
96	aaaagaaaga	agaggccaaa	aaagaagatg	aagatgaggt	accagatgga	ccaaaaccaa	2280
98	tgctgccata	ttcgtccatg	tttattttgt	cacctactaa	tccaattagg	cgaggcgcac	2340
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106	acctcgcat	cctgttccac	ccgggcgect	acctgcgcga	cctgtggaac	atcatggatg	2580
108	ccgccgtcgt	catatgcgcc	cttgtcagct	tcggatttga	gatcgagggc	gtgaaaaagg	2640
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112	tgaaaactat	aaaacgagtt	ccaaagttaa	aagcagtgtt	tgactgtgtt	gtgaactctt	2760
114	tgaaaaacgt	cattaacatt	ctcattgtgt	acatattgtt	tcaattcata	ttcgtgttaa	2820
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118	ttgaagactg	ccaagggctg	tatttcgtgt	acgagtcaaa	cagcttgctg	ccgaaagtca	2940
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124	ccacctacga	agacagggga	cccatacaaa	attttcgaat	agaaatgtcc	atattttata	3120
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128	tcacatttca	agagcagggc	gaagctgagc	ttcaggatgg	tgaaattgat	aagaatcaga	3240
130	aatcgtgtat	agacttcacg	atagaagcgc	gacctctcga	gaggtatatg	ccaagcaaaa	3300
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134	tcatgacgct	gatcgtcttc	aacacattgt	tgctcatgat	gaagtttcac	gaggctccac	3420
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140	cattcgattt	tattacggtc	attggaagta	ttattgacgc	cctcattatg	gagtttggcg	3600
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148	aggtgttttg	caatatagaa	ttaacaccag	agtctgacat	gaacagacac	aacaattttc	3840
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152	acataatgtt	ggcttgccgc	aaacccgcca	agtgcgacat	agcagctgga	aaggcctcca	3960
154	acgaagaatg	tggaagtacg	ctcgcctacg	cctacttcgt	atcttttata	ttcttctgtt	4020
156	cgtttcttat	gttgaatttg	ttcgttgctg	ttattatgga	taactttgac	tacctaacga	4080
158	gggactcgtc	catcctcggc	gcacatcatc	ttgatgaatt	tgtagaata	tgggcagaat	4140
160	atgatccaaa	cgccacgggt	aagatccatt	atacagaaat	gtatgatatg	ttgaagaata	4200
162	tggatccgcc	tctgggggtt	ggtaacaaat	gtccaaatag	actagcatat	aagaagctta	4260
164	ttagaatgaa	tatgccgcta	gacgatgagg	ggaaagttaa	ttttacaaca	acactatttg	4320
166	ccttaatacg	agaaaaactg	aacatcaaaa	tgagatctcc	cgaggaaatg	gaccaagcag	4380
168	atgaggaatt	aagggaacaa	ataaccacaa	tttgccatt	acaagcgaag	aagatgctcg	4440
170	acctgctggt	gcctcgaaac	gatgtactca	acgctggaaa	actgaccgtc	gggaagatat	4500
172	acgctggact	tctaactctc	gagagttgga	gatctacaag	gttcaagcag	aatggtgttc	4560
174	cggtagtggg	actacaagga	tcacaccacg	cctcaatgga	gtcgttggac	gagggacggt	4620

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Input Set : A:\60290-USA Sequence Listing.txt

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176 tacaagctcc tcacacgtac cagaatggac accaccatgg gagatcatcc agtttaagac 4680
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180 cagacaccgt cagcaacgtc gtcgagatag taaagcatga acaccagaga cacgggcgaa 4800
182 cgcacagagc gcccactac taccacccac atgtttgggc cccgataggt gagcgggagc 4860
184 gggaccgcga gtggcgggag tggcgcgacc gctcctggga gcgcgagggc gcgcgccgcg 4920
186 gccgcggccg ccagttgccc cccacgcca ccaagccgtc cacgctacag gtcaagcagc 4980
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190 gagaacc 5047
193 <210> SEQ ID NO: 2
194 <211> LENGTH: 1662
195 <212> TYPE: PRT
196 <213> ORGANISM: Heliothis virescens
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204 Ile Phe Ala Asp Glu Asn Pro Ile Arg Arg Tyr Thr Lys Phe Ile Ile
205 20 25 30
208 Glu Trp Pro Pro Phe Glu Tyr Ala Val Leu Leu Thr Ile Ala Asn
209 35 40 45
212 Cys Val Val Leu Ala Leu Glu Glu His Leu Pro Asn Gly Asp Lys Thr
213 50 55 60
216 Ile Leu Ala Gln Asn Leu Glu Lys Thr Glu Ala Tyr Phe Leu Gly Ile
217 65 70 75 80
220 Phe Cys Val Glu Ala Ser Leu Lys Ile Leu Ala Leu Gly Phe Val Leu
221 85 90 95
224 His Arg Gly Ser Tyr Leu Arg Asn Val Trp Asn Ile Met Asp Phe Phe
225 100 105 110
228 Val Val Val Thr Gly Ile Ile Thr Gln Leu Pro Ile Ala Pro Ala Asp
229 115 120 125
232 Val Asp Phe Arg Thr Leu Arg Ala Ile Arg Val Leu Arg Pro Leu Lys
233 130 135 140
236 Leu Val Ser Gly Val Pro Ser Leu Gln Val Val Leu Lys Ser Ile Ile
237 145 150 155 160
240 Lys Ala Met Ala Pro Leu Leu Gln Ile Gly Leu Leu Val Leu Phe Ala
241 165 170 175
244 Ile Val Ile Phe Ala Ile Ile Gly Leu Glu Phe Tyr Ser Gly Ala Leu
245 180 185 190
248 His Lys Thr Cys Tyr Asn Leu Glu Asp Ile Ser Glu Ile Val Asn Glu
249 195 200 205
252 Gly Asp Ser Ala Thr Pro Cys Asn Ala Asp Asn Val Ser Leu Ala Pro
253 210 215 220
256 Phe Gly Ala Asn Val Cys Asp Tyr Glu Lys Ser Thr Cys Leu Glu Lys
257 225 230 235 240
260 Trp Glu Gly Pro Asn Arg Gly Ile Thr Ser Phe Asp Asn Ile Gly Phe
261 245 250 255
264 Ala Met Leu Thr Val Phe Gln Cys Ile Thr Met Glu Gly Trp Thr Ala
265 260 265 270
268 Ile Leu Tyr Trp Thr Asn Asp Ala Leu Gly Ser Ala Phe Asn Trp Ile
269 275 280 285

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272 Tyr Phe Val Pro Leu Ile Val Leu Gly Ser Phe Phe Met Leu Asn Leu
273      290      295      300
276 Val Leu Gly Val Leu Ser Gly Glu Phe Ala Lys Glu Arg Glu Lys Val
277 305      310      315      320
280 Glu Asn Arg Gln Glu Phe Leu Lys Leu Arg Arg Gln Gln Gln Leu Glu
281      325      330      335
284 Arg Glu Leu Asn Gly Tyr Val Glu Trp Ile Cys Lys Ala Glu Glu Val
285      340      345      350
288 Ile Leu Ala Glu Glu Arg Thr Thr Glu Glu Glu Lys Met His Ile Ile
289      355      360      365
292 Glu Ala Arg Arg Arg Ala Ala Ala Lys Lys Lys Leu Lys Asn Leu Gly
293      370      375      380
296 Lys Ser Lys Ser Thr Asp Thr Glu Glu Glu Glu Gln Asp Glu Asp Cys
297 385      390      395      400
300 Gly Asp Asp Gly Phe Leu Lys Ser Lys Ala Arg Ser Ala Gly Arg Phe
301      405      410      415
304 Ala Asp Phe Trp Arg Ala Glu Lys Arg Phe Arg Phe Trp Ile Arg His
305      420      425      430
308 Thr Val Lys Thr Gln Trp Phe Tyr Trp Phe Val Ile Val Leu Val Leu
309      435      440      445
312 Phe Asn Thr Ile Cys Val Ala Val Glu His Tyr Arg Gln Pro Lys Trp
313      450      455      460
316 Leu Thr Ser Phe Leu Tyr Tyr Ala Glu Phe Val Phe Leu Gly Leu Phe
317 465      470      475      480
320 Met Met Glu Met Trp Val Lys Met Tyr Ala Leu Gly Pro Arg Ile Tyr
321      485      490      495
324 Phe Glu Ser Ser Phe Asn Arg Phe Asp Cys Val Val Ile Ser Gly Ser
325      500      505      510
328 Ile Phe Glu Val Val Trp Ser Glu Val Lys Gly Gly Ser Phe Gly Leu
329      515      520      525
332 Ser Val Leu Arg Ala Leu Arg Leu Leu Arg Ile Phe Lys Val Thr Lys
333      530      535      540
336 Tyr Trp Ser Ser Leu Arg Asn Leu Val Ile Ser Leu Leu Asn Ser Met
337 545      550      555      560
340 Arg Ser Ile Ile Ser Leu Leu Phe Leu Leu Phe Leu Phe Ile Leu Ile
341      565      570      575
344 Phe Ala Leu Leu Gly Met Gln Leu Phe Gly Gly Gln Phe Asn Phe Glu
345      580      585      590
348 Asp Gly Thr Pro Pro Thr Asn Phe Asn Thr Phe Pro Ile Ala Leu Leu
349      595      600      605
352 Thr Val Phe Gln Ile Leu Thr Gly Glu Asp Trp Asn Glu Val Met Tyr
353      610      615      620
356 Asp Gly Ile Gln Ser Gln Gly Gly Ile Gln Arg Gly Met Ile Tyr Ser
357 625      630      635      640
360 Leu Tyr Phe Val Ile Leu Val Leu Phe Gly Asn Tyr Thr Leu Leu Asn
361      645      650      655
364 Val Phe Leu Ala Ile Ala Val Asp Asn Leu Ala Asn Ala Gln Glu Leu
365      660      665      670
368 Thr Ala Ala Glu Glu Glu Gln Val Glu Glu Asp Lys Glu Lys Gln Leu

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369          675          680          685
372 Gln Glu Leu Glu Lys Gly Met Gly Ala Leu His Ala Val Asp Gly Thr
373          690          695          700
376 Pro Pro Gly Val Asp Leu Ser Pro Ser Ser Pro Thr Ser Arg Lys Asn
377 705          710          715          720
380 Lys Lys Lys Glu Glu Ala Lys Lys Glu Asp Glu Asp Glu Val Pro Asp
381          725          730          735
384 Gly Pro Lys Pro Met Leu Pro Tyr Ser Ser Met Phe Ile Leu Ser Pro
385          740          745          750
388 Thr Asn Pro Ile Arg Arg Gly Ala His Trp Val Val Asn Leu Arg Tyr
389          755          760          765
392 Phe Asp Phe Phe Ile Met Val Val Ile Cys Met Ser Ser Ala Ala Leu
393          770          775          780
396 Ala Ala Glu Asp Pro Val Val Glu Glu Ser Asp Arg Asn Lys Ile Leu
397 785          790          795          800
400 Asn Tyr Phe Asp Tyr Ala Phe Thr Gly Val Phe Thr Val Glu Met Leu
401          805          810          815
404 Leu Lys Ile Val Asp Leu Gly Ile Leu Phe His Pro Gly Ala Tyr Leu
405          820          825          830
408 Arg Asp Leu Trp Asn Ile Met Asp Ala Ala Val Val Ile Cys Ala Leu
409          835          840          845
412 Val Ser Phe Gly Phe Glu Ile Gly Gly Val Lys Lys Gly Ala Gly Gln
413          850          855          860
416 Asn Leu Ser Thr Ile Lys Ser Leu Arg Val Leu Arg Val Leu Arg Pro
417 865          870          875          880
420 Leu Lys Thr Ile Lys Arg Val Pro Lys Leu Lys Ala Val Phe Asp Cys
421          885          890          895
424 Val Val Asn Ser Leu Lys Asn Val Ile Asn Ile Leu Ile Val Tyr Ile
425          900          905          910
428 Leu Phe Gln Phe Ile Phe Ala Val Ile Ala Val Gln Leu Phe Asn Gly
429          915          920          925
432 Lys Phe Phe His Cys Asn Asp Ile Ser Lys Asn Thr Phe Glu Asp Cys
433          930          935          940
436 Gln Gly Ser Tyr Phe Val Tyr Glu Ser Asn Ser Leu Leu Pro Lys Val
437 945          950          955          960
440 Asn Gln Arg Thr Trp Thr Thr Gln Ser Phe His Tyr Asp Asn Val Ala
441          965          970          975
444 Val Ala Met Leu Thr Leu Phe Ala Val Gln Thr Gly Glu Gly Trp Pro
445          980          985          990
448 Gln Val Leu Gln Asn Ser Met Ala Ala Thr Tyr Glu Asp Arg Gly Pro
449          995          1000          1005
452 Ile Gln Asn Phe Arg Ile Glu Met Ser Ile Phe Tyr Ile Val Tyr
453          1010          1015          1020
456 Phe Val Val Phe Pro Phe Phe Phe Val Asn Ile Phe Val Ala Leu
457          1025          1030          1035
460 Ile Ile Ile Thr Phe Gln Glu Gln Gly Glu Ala Glu Leu Gln Asp
461          1040          1045          1050
464 Gly Glu Ile Asp Lys Asn Gln Lys Ser Cys Ile Asp Phe Thr Ile
465          1055          1060          1065

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : A:\60290-USA Sequence Listing.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 35
Seq#:21; N Pos. 1
Seq#:22; N Pos. 25,31
Seq#:49; N Pos. 18,24
Seq#:65; N Pos. 27
Seq#:67; N Pos. 20
Seq#:77; N Pos. 15,18

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:19; Line(s) 3492

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42
Seq#:43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66
Seq#:67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:3521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:3544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:3898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:4109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0
L:4140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
L:4276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0